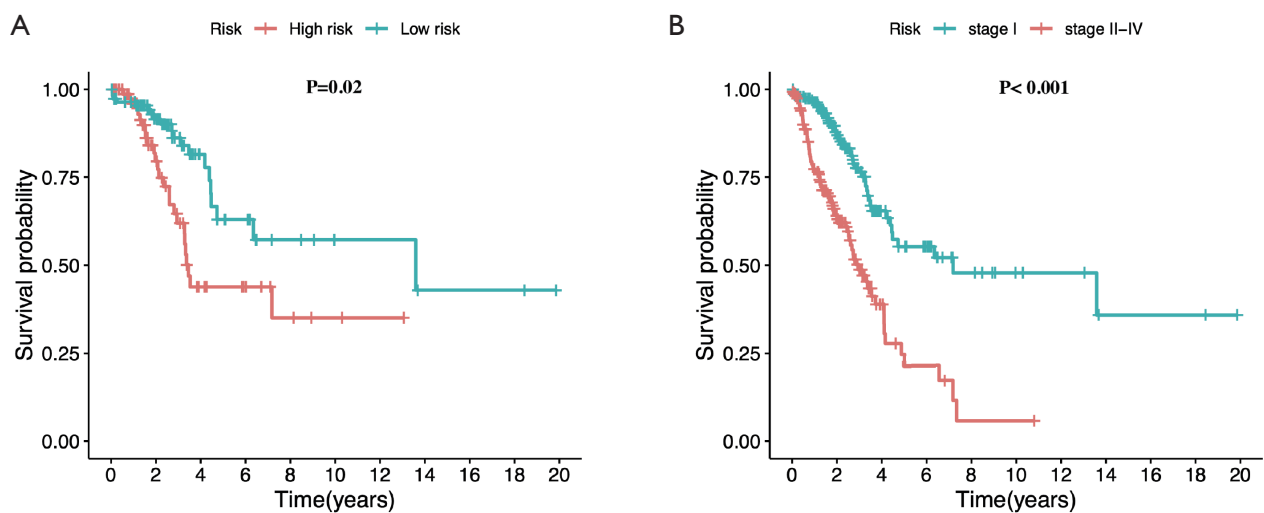
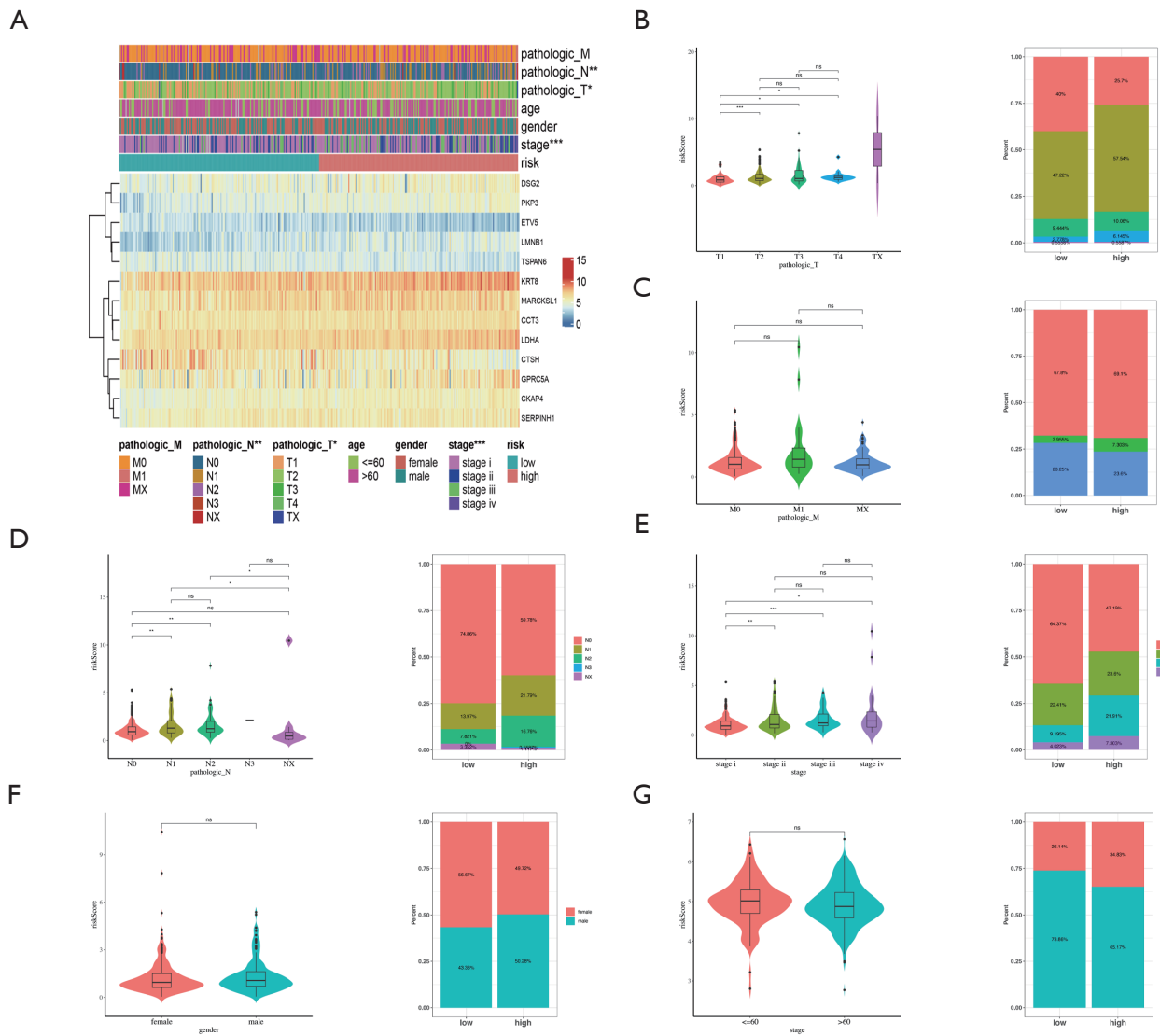


**Table S1** The sequence of primers (5'-3')

| Gene            | Type             | Sequence                 |
|-----------------|------------------|--------------------------|
| <i>CCT3</i>     | Forward sequence | GGAGGAAGAGTACATCCAGCAG   |
|                 | Reverse sequence | CCGCATAAGGTAGTGCTGAGCT   |
| <i>CKAP4</i>    | Forward sequence | TTTCTCGGGCTGGTGCGTCCA    |
|                 | Reverse sequence | GGACTCAAAAGTTCCAAATGTGGC |
| <i>CTSH</i>     | Forward sequence | TACCTTCGAGGTACTGGTCCCT   |
|                 | Reverse sequence | GGTGGAGAAAGTCCAGCAACTG   |
| <i>DSG2</i>     | Forward sequence | AGGGAAGCACAGCATGACTCCT   |
|                 | Reverse sequence | CCTTTCGCAATGGCACATCAG    |
| <i>ETV5</i>     | Forward sequence | GTGTTGTGCCTGAGAGACTGGA   |
|                 | Reverse sequence | CGACCTGTCCAGGCAATGAAGT   |
| <i>GPRC5A</i>   | Forward sequence | GCTATGGTGTGGAGAACAGAGC   |
|                 | Reverse sequence | GCAGCTGAAAATGTGTGGAATAGG |
| <i>KRT8</i>     | Forward sequence | ACAAGGTAGAGCTGGAGTCTCG   |
|                 | Reverse sequence | AGCACCACAGATGTGTCCGAGA   |
| <i>LDHA</i>     | Forward sequence | GGATCTCCAACATGGCAGCCTT   |
|                 | Reverse sequence | AGACGGCTTTCTCCCTCTTGCT   |
| <i>MARCKSL1</i> | Forward sequence | CAGGCTACAGAGCCATCCACTC   |
|                 | Reverse sequence | GCAGCTTAGAGATCACCCACCT   |
| <i>PKP3</i>     | Forward sequence | GCCTACATCCAGCACAAAGTGCT  |
|                 | Reverse sequence | GCGTTGTGCTAGATGAGGTTGC   |
| <i>SERPINH1</i> | Forward sequence | AACCGTGGCTTCATGGTGACTC   |
|                 | Reverse sequence | TGATGAGGCTGGAGAGCTTGTG   |
| <i>TSPAN6</i>   | Forward sequence | CGTGCTCATTGCTACTGGTACC   |
|                 | Reverse sequence | CAAATCCTACGATGGCAGCGAC   |

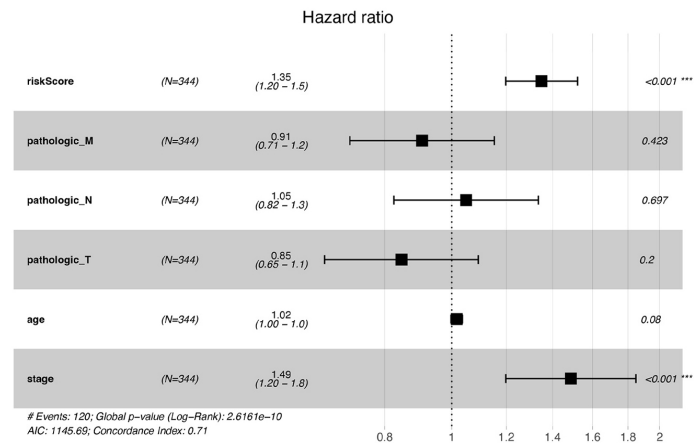


**Figure S1** Clinical validity in stage I LUAD patient. (A) It shows the survival difference among 196 patients with stage I disease, with 84 cases in the high-risk group and 112 cases in the low-risk group. (B) It presents the results of the survival stratification analysis of all patients by stage, indicating that patients in stages II–IV have significantly lower survival compared to those in stage I.

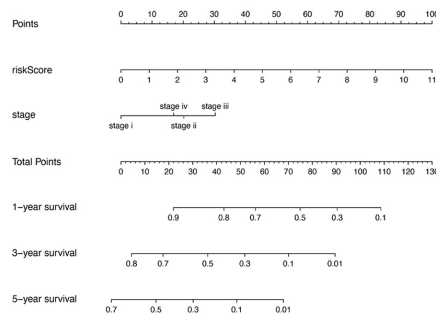


**Figure S2** Associations observed between risk model and clinicopathological features. (A) Heatmap of different clinicopathological subtype features. (B-G) Comparison of pathological stage T, M, N, stage, gender, and age between two groups with violin plots and intergroup proportion bar plots. \*,  $P < 0.05$ ; \*\*,  $P < 0.01$ ; \*\*\*,  $P < 0.001$ ; ns, not statistically significant.

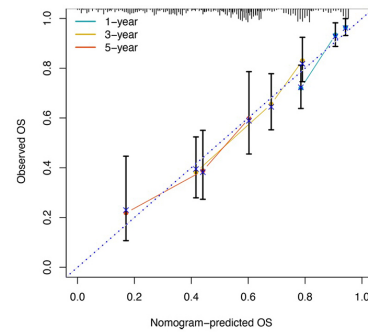
A



B



C



**Figure S3** Construction of the nomograph model. (A) Univariate Cox regression forest plot of clinical information. (B) Nomogram plot of the independent prognostic factor survival prediction model. (C) Calibration curve. \*\*\*,  $P < 0.001$ .